

RAW SEQUENCE LISTING

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Application Serial Number: 10/580,141
Source: JFW
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RAW SEQUENCE LISTING

DATE: 04/20/2007

PATENT APPLICATION: US/10/580,141

TIME: 11:19:31

Input Set : E:\10-580141.txt

Output Set: N:\CRF4\04202007\J580141.raw

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3 <110> APPLICANT: Aventis Pasteur Limited
4   Brunham, Robert
5   Raudonikiene, Ausra
6   Gallichan, Scott
7   Murdin, Andrew
9 <120> TITLE OF INVENTION: Immunization Against Chlamydia Infectio with 60K CRMP
11 <130> FILE REFERENCE: RY185
13 <140> CURRENT APPLICATION NUMBER: US 10/580,141
14 <141> CURRENT FILING DATE: 2006-05-19
16 <150> PRIOR APPLICATION NUMBER: US 60/481,676
17 <151> PRIOR FILING DATE: 2003-11-20
19 <150> PRIOR APPLICATION NUMBER: PCT/CA2004/002004
20 <151> PRIOR FILING DATE: 2004-11-22
23 <160> NUMBER OF SEQ ID NOS: 14
25 <170> SOFTWARE: PatentIn version 3.3
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1662
29 <212> TYPE: DNA
30 <213> ORGANISM: Chlamydia muridium
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)..(1662)
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40 1          5          10          15
42 atc ttc gcg gtg act agt gtg gcg agt tta ttt gct agc ggg gtg tta      96
43 Ile Phe Ala Val Thr Ser Val Ala Ser Leu Phe Ala Ser Gly Val Leu
44          20          25          30
46 gag acc tct atg gca gag tct ctc tct acc aac gtt att agc tta gct      144
47 Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala
48          35          40          45
50 gac acc aaa gcg aaa gag acc act tct cat caa aaa gac aga aaa gca      192
51 Asp Thr Lys Ala Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala
52          50          55          60
54 aga aaa aat cat caa aat agg act tcc gta gtc cgt aaa gag gtt act      240
55 Arg Lys Asn His Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr
56 65          70          75          80
58 gca gtt cgt gat act aaa gct gta gag cct aga cag gat tct tgc ttt      288
59 Ala Val Arg Asp Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe
60          85          90          95
62 ggc aaa atg tat aca gtc aaa gtt aat gat gat cgt aat gta gaa atc      336
63 Gly Lys Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile

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64	100	105	110	
66	gtg cag tcc gtt cct gaa tat gct acg gta gga tct cca tat cct att	384		
67	Val Gln Ser Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile			
68	115 120 125			
70	gag att act gct ata ggg aaa aga gac tgt gtt gat gta atc att aca	432		
71	Glu Ile Thr Ala Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr			
72	130 135 140			
74	cag caa tta cca tgc gaa gca gag ttt gtt agc agt gat cca gct act	480		
75	Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Ser Ser Asp Pro Ala Thr			
76	145 150 155 160			
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79	Thr Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly			
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82	cag ggc gaa aag agt aaa att act gta tgg gta aaa cct ctt aaa gaa	576		
83	Gln Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu			
84	180 185 190			
86	ggt tgc tgc ttt aca gct gca acg gtt tgt gct tgt cca gag atc cgt	624		
87	Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg			
88	195 200 205			
90	tcg gtt acg aaa tgt ggc cag cct gct atc tgt gtt aaa cag gaa ggt	672		
91	Ser Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly			
92	210 215 220			
94	cca gaa agc gca tgt ttg cgt tgc cca gta act tat aga att aat gta	720		
95	Pro Glu Ser Ala Cys Leu Arg Cys Pro Val Thr Tyr Arg Ile Asn Val			
96	225 230 235 240			
98	gtc aac caa gga aca gca aca gca cgt aat gtt gtt gtg gaa aat cct	768		
99	Val Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro			
100	245 250 255			
102	gtt cca gat ggc tat gct cat gca tcc gga cag cgt gta ttg aca tat	816		
103	Val Pro Asp Gly Tyr Ala His Ala Ser Gly Gln Arg Val Leu Thr Tyr			
104	260 265 270			
106	act ctt ggg gat atg caa cct gga gaa cag aga aca atc acc gtg gag	864		
107	Thr Leu Gly Asp Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu			
108	275 280 285			
110	ttt tgt ccg ctt aaa cgt ggt cga gtc aca aat att gct aca gtt tct	912		
111	Phe Cys Pro Leu Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser			
112	290 295 300			
114	tac tgt ggt gga cac aaa aat act gct agc gta aca aca gtg atc aat	960		
115	Tyr Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn			
116	305 310 315 320			
118	gag cct tgc gtg caa gtt aac atc gag gga gca gat tgg tct tat gtt	1008		
119	Glu Pro Cys Val Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val			
120	325 330 335			
122	tgt aag cct gta gaa tat gtt atc tct gtt tct aac cct ggt gac tta	1056		
123	Cys Lys Pro Val Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu			
124	340 345 350			
126	gtt tta cga gac gtt gta att gaa gat acg ctt tct cct gga ata act	1104		
127	Val Leu Arg Asp Val Val Ile Glu Asp Thr Leu Ser Pro Gly Ile Thr			
128	355 360 365			

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130 gtt gtt gaa gca gct gga gct cag att tct tgt aat aaa ttg gtt tgg      1152
131 Val Val Glu Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp
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134 act ttg aag gaa ctc aat cct gga gag tct tta caa tat aag gtt cta      1200
135 Thr Leu Lys Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu
136 385                      390                      395                      400
138 gta aga gct caa act cca ggg caa ttc aca aac aac gtt gtt gtg aaa      1248
139 Val Arg Ala Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys
140                      405                      410                      415
142 agt tgc tct gat tgc ggt att tgt act tct tgc gca gaa gca aca act      1296
143 Ser Cys Ser Asp Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr
144                      420                      425                      430
146 tac tgg aaa gga gtt gct gct act cat atg tgc gta gta gat act tgt      1344
147 Tyr Trp Lys Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys
148                      435                      440                      445
150 gat cct att tgc gta gga gag aac act gtt tat cgt atc tgt gtg aca      1392
151 Asp Pro Ile Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr
152 450                      455                      460
154 aac aga ggt tct gct gaa gat aca aat gtg tcc tta att ttg aaa ttc      1440
155 Asn Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Ile Leu Lys Phe
156 465                      470                      475                      480
158 tct aaa gaa tta caa cct ata tct ttc tct gga cca act aaa gga acc      1488
159 Ser Lys Glu Leu Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr
160                      485                      490                      495
162 att aca gga aac acg gta gtg ttt gat tgc tta cct aga tta ggt tct      1536
163 Ile Thr Gly Asn Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser
164                      500                      505                      510
166 aaa gaa act gta gag ttt tct gta acg ttg aaa gca gta tcc gct gga      1584
167 Lys Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly
168                      515                      520                      525
170 gat gct cgt ggg gaa gct att ctt tct tcc gat aca ttg aca gtt cct      1632
171 Asp Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro
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181 <212> TYPE: PRT
182 <213> ORGANISM: Chlamydia muridium
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191                      20                      25                      30
194 Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala
195                      35                      40                      45
198 Asp Thr Lys Ala Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala
199 50                      55                      60

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202 Arg Lys Asn His Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr
203 65 70 75 80
206 Ala Val Arg Asp Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe
207 85 90 95
210 Gly Lys Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile
211 100 105 110
214 Val Gln Ser Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile
215 115 120 125
218 Glu Ile Thr Ala Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr
219 130 135 140
222 Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Ser Ser Asp Pro Ala Thr
223 145 150 155 160
226 Thr Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly
227 165 170 175
230 Gln Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu
231 180 185 190
234 Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg
235 195 200 205
238 Ser Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly
239 210 215 220
242 Pro Glu Ser Ala Cys Leu Arg Cys Pro Val Thr Tyr Arg Ile Asn Val
243 225 230 235 240
246 Val Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro
247 245 250 255
250 Val Pro Asp Gly Tyr Ala His Ala Ser Gly Gln Arg Val Leu Thr Tyr
251 260 265 270
254 Thr Leu Gly Asp Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu
255 275 280 285
258 Phe Cys Pro Leu Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser
259 290 295 300
262 Tyr Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn
263 305 310 315 320
266 Glu Pro Cys Val Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val
267 325 330 335
270 Cys Lys Pro Val Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu
271 340 345 350
274 Val Leu Arg Asp Val Val Ile Glu Asp Thr Leu Ser Pro Gly Ile Thr
275 355 360 365
278 Val Val Glu Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp
279 370 375 380
282 Thr Leu Lys Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu
283 385 390 395 400
286 Val Arg Ala Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys
287 405 410 415
290 Ser Cys Ser Asp Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr
291 420 425 430
294 Tyr Trp Lys Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys
295 435 440 445
298 Asp Pro Ile Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr

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299      450      455      460
302 Asn Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Ile Leu Lys Phe
303 465      470      475      480
306 Ser Lys Glu Leu Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr
307      485      490      495
310 Ile Thr Gly Asn Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser
311      500      505      510
314 Lys Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly
315      515      520      525
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327 <211> LENGTH: 1659
328 <212> TYPE: DNA
329 <213> ORGANISM: Chlamydia trachomatis
332 <220> FEATURE:
333 <221> NAME/KEY: CDS
334 <222> LOCATION: (1)..(1659)
336 <400> SEQUENCE: 3
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338 Met Arg Ile Gly Asp Pro Met Asn Lys Leu Ile Arg Arg Ala Val Thr
339 1      5      10      15
341 atc ttc gcg gtg act agt gtg gcg agt tta ttt gct agc ggg gtg tta      96
342 Ile Phe Ala Val Thr Ser Val Ala Ser Leu Phe Ala Ser Gly Val Leu
343      20      25      30
345 gag acc tct atg gca gag tct ctc tct aca aac gtt att agc tta gct      144
346 Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala
347      35      40      45
349 gac acc aaa gcg aaa gac aac act tct cat aaa agc aaa aaa gca aga      192
350 Asp Thr Lys Ala Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg
351 50      55      60
353 aaa aac cac agc aaa gag act ccc gta gac cgt aaa gag gtt gct ccg      240
354 Lys Asn His Ser Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro
355 65      70      75      80
357 gtt cat gag tct aaa gct aca gga cct aaa cag gat tct tgc ttt ggc      288
358 Val His Glu Ser Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly
359      85      90      95
361 aga atg tat aca gtc aaa gtt aat gat gat cgc aat gtt gaa atc aca      336
362 Arg Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr
363      100      105      110
365 caa gct gtt cct gaa tat gct acg gta gga tct ccc tat cct att gaa      384
366 Gln Ala Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu
367      115      120      125
369 att act gct aca ggt aaa agg gat tgt gtt gat gtt atc att act cag      432
370 Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln
371 130      135      140
373 caa tta cca tgt gaa gca gag ttc gta cgc agt gat cca gcg aca act      480

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VERIFICATION SUMMARY

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